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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/782,874
DATE: 04/26/2001
TIME: 17:23:37

Input Set : N:\Crf3\RULE60\09782874.txt
Output Set: N:\CRF3\04262001\I782874.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Wassenegger, Michael
7 Riedel, Leonhard
8 Schiebel, Winfried
9 Sanger, Heinz
11 (ii) TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
12 POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
13 RNA-DIRECTED RNA POLYMERASE (RdRP)
15 (iii) NUMBER OF SEQUENCES: 13
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: FISH & NEAVE
19 (B) STREET: 1251 Avenue of the Americas
20 (C) CITY: New York
21 (D) STATE: New York
22 (E) COUNTRY: USA
23 (F) ZIP: 10020
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
31 (vi) CURRENT APPLICATION DATA:
C--> 32 (A) APPLICATION NUMBER: US/09/782,874
C--> 33 (B) FILING DATE: 08-Feb-2001
34 (C) CLASSIFICATION:
36 (vii) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: US 08/811,583
38 (B) FILING DATE: 05-MAR-1997
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: Haley, James F.
43 (B) REGISTRATION NUMBER: 27,794
44 (C) REFERENCE/DOCKET NUMBER: MPG-1
46 (ix) TELECOMMUNICATION INFORMATION:
47 (A) TELEPHONE: 212-596-9000
48 (B) TELEFAX: 212-596-9090
51 (2) INFORMATION FOR SEQ ID NO: 1:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 3731 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
59 (ii) MOLECULE TYPE: cDNA
61 (vi) ORIGINAL SOURCE:
62 (A) ORGANISM: Tomato
64 (ix) FEATURE:
65 (A) NAME/KEY: CDS

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66      (B) LOCATION: 194..3535
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71  GAAATATTCT TTA CTTACTT CACCAGGGAT TGACTCATCA CTCCCCTCAA GTCTTTGTGT      60
73  GTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCACTCAC TACTGCTGGG TAGTTTTTAT      120
75  TTTGCATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG AACTGCACTT      180
77  GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GGA TTC CCT TAT      229
78      Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr
79      1          5          10
81  CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA      277
82  Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly
83      15          20          25
85  TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT      325
86  Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser
87      30          35          40
89  AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA      373
90  Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys
91      45          50          55          60
93  ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG      421
94  Ile Ile Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu
95      65          70          75
97  AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG      469
98  Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val
99      80          85          90
101 GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT      517
102 Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp
103      95          100          105
105 GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC      565
106 Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly
107      110          115          120
109 ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC      613
110 Ile Gly Leu Lys Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp
111      125          130          135          140
113 TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT      661
114 Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His
115      145          150          155
117 CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT      709
118 Arg Pro Tyr Gly Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly
119      160          165          170
121 GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT      757
122 Ala Pro Arg Ile Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe
123      175          180          185
125 AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA      805
126 Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro
127      190          195          200
129 TCT TGG ATA GGG CTA TCT TCT AGC TTA TGT TTG CAG TTC CGT AGG GGT      853
130 Ser Trp Ile Gly Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly
131      205          210          215          220
133 GTT CGT CTT CCA AAT TTC GAG GAA AGT TTT TTC CAC TAT GCA GAA CGT      901
134 Val Arg Leu Pro Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg

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135		225		230		235	
137	GAA AAC AAT ATT ACT TTA CAG ACT GGT TTC ACC TTT TTC GTC TCT CAA						949
138	Glu Asn Asn Ile Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln						
139		240		245		250	
141	AAA TCG GCT CTG GTT CCC AAT GTC CAG CCT CCG GAA GGA ATT TCA ATT						997
142	Lys Ser Ala Leu Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile						
143		255		260		265	
145	CCC TAC AAG ATT TTG TTC AAA ATT AGT TCT TTG GTA CAG CAT GGA TGC						1045
146	Pro Tyr Lys Ile Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys						
147		270		275		280	
149	ATA CCT GGG CCA GCA TTA AAT GTC TAC TTT TTC CGA TTA GTT GAT CCT						1093
150	Ile Pro Gly Pro Ala Leu Asn Val Tyr Phe Phe Arg Leu Val Asp Pro						
151	285		290		295	300	
153	CGA AGG AGA AAT GTG GCA TGC ATT GAG CAT GCC TTA GAG AAA CTG TAC						1141
154	Arg Arg Arg Asn Val Ala Cys Ile Glu His Ala Leu Glu Lys Leu Tyr						
155		305		310		315	
157	TAT ATA AAG GAG TGC TGT TAT GAT CCC GTG AGG TGG CTC ACT GAG CAG						1189
158	Tyr Ile Lys Glu Cys Cys Tyr Asp Pro Val Arg Trp Leu Thr Glu Gln						
159		320		325		330	
161	TAT GAT GGG TAT CTC AAG GGT AGA CAA CCT CCA AAA TCT CCG TCC ATC						1237
162	Tyr Asp Gly Tyr Leu Lys Gly Arg Gln Pro Pro Lys Ser Pro Ser Ile						
163		335		340		345	
165	ACT TTA GAT GAT GGG TTG GTG TAT GTA AGA AGG GTC CTA GTA ACA CCA						1285
166	Thr Leu Asp Asp Gly Leu Val Tyr Val Arg Arg Val Leu Val Thr Pro						
167		350		355		360	
169	TGC AAA GTT TAT TTT TGT GGT CCA GAG GTT AAT GTT TCC AAT CGG GTT						1333
170	Cys Lys Val Tyr Phe Cys Gly Pro Glu Val Asn Val Ser Asn Arg Val						
171	365		370		375	380	
173	CTC CGC AAT TAT TCT GAA GAC ATA GAT AAC TTT CTT CGT GTT TCT TTT						1381
174	Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn Phe Leu Arg Val Ser Phe						
175		385		390		395	
177	GTT GAT GAG GAG TGG GAG AAA CTG TAT TCT ACA GAC TTA TTA CCA AAA						1429
178	Val Asp Glu Glu Trp Glu Lys Leu Tyr Ser Thr Asp Leu Leu Pro Lys						
179		400		405		410	
181	GCA AGT ACT GGA AGT GGT GTC AGG ACA AAC ATC TAT GAG AGG ATC TTA						1477
182	Ala Ser Thr Gly Ser Gly Val Arg Thr Asn Ile Tyr Glu Arg Ile Leu						
183		415		420		425	
185	TCA ACT CTG CGG AAA GGC TTT GTA ATT GGT GAT AAA AAA TTT GAA TTT						1525
186	Ser Thr Leu Arg Lys Gly Phe Val Ile Gly Asp Lys Lys Phe Glu Phe						
187		430		435		440	
189	CTT GCA TTT TCA TCG AGC CAG TTG CGG GAT AAT TCA GTG TGG ATG TTT						1573
190	Leu Ala Phe Ser Ser Ser Gln Leu Arg Asp Asn Ser Val Trp Met Phe						
191	445		450		455	460	
193	GCA TCA AGA CCT GGC CTT ACT GCA AAT GAT ATA AGA GCT TGG ATG GGT						1621
194	Ala Ser Arg Pro Gly Leu Thr Ala Asn Asp Ile Arg Ala Trp Met Gly						
195		465		470		475	
197	GAT TTT TCG CAG ATC AAG AAT GTC GCA AAA TAT GCT GCC AGA CTT GGT						1669
198	Asp Phe Ser Gln Ile Lys Asn Val Ala Lys Tyr Ala Ala Arg Leu Gly						
199		480		485		490	

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201	CAA	TCT	TTT	GGT	TCC	TCC	AGA	GAG	ACT	TTG	AGT	GTT	CTT	AGG	CAT	GAG	1717
202	Gln	Ser	Phe	Gly	Ser	Ser	Arg	Glu	Thr	Leu	Ser	Val	Leu	Arg	His	Glu	
203			495					500					505				
205	ATT	GAA	GTT	ATT	CCC	GAT	GTA	AAG	GTT	CAT	GGA	ACC	AGC	TAT	GTC	TTT	1765
206	Ile	Glu	Val	Ile	Pro	Asp	Val	Lys	Val	His	Gly	Thr	Ser	Tyr	Val	Phe	
207			510					515					520				
209	TCT	GAT	GGA	ATT	GGT	AAA	ATA	TCT	GGT	GAC	TTT	GCT	CAT	AGA	GTT	GCC	1813
210	Ser	Asp	Gly	Ile	Gly	Lys	Ile	Ser	Gly	Asp	Phe	Ala	His	Arg	Val	Ala	
211	525						530					535				540	
213	TCA	AAA	TGT	GGC	CTT	CAA	TAT	ACC	CCA	TCT	GCT	TTC	CAG	ATT	CGT	TAT	1861
214	Ser	Lys	Cys	Gly	Leu	Gln	Tyr	Thr	Pro	Ser	Ala	Phe	Gln	Ile	Arg	Tyr	
215						545					550				555		
217	GGT	GGA	TAT	AAA	GGT	GTT	GTG	GGT	GTT	GAT	CCG	GAT	TCA	TCA	ATG	AAG	1909
218	Gly	Gly	Tyr	Lys	Gly	Val	Val	Gly	Val	Asp	Pro	Asp	Ser	Ser	Met	Lys	
219				560						565					570		
221	TTG	TCT	TTG	AGA	AAG	AGC	ATG	TCG	AAA	TAT	GAA	TCA	GAC	AAC	ATA	AAG	1957
222	Leu	Ser	Leu	Arg	Lys	Ser	Met	Ser	Lys	Tyr	Glu	Ser	Asp	Asn	Ile	Lys	
223				575						580					585		
225	TTA	GAT	GTC	CTT	GGA	TGG	AGC	AAA	TAT	CAG	CCT	TGT	TAT	CTT	AAT	CGT	2005
226	Leu	Asp	Val	Leu	Gly	Trp	Ser	Lys	Tyr	Gln	Pro	Cys	Tyr	Leu	Asn	Arg	
227				590						595					600		
229	CAA	CTG	ATT	ACG	CTC	TTG	TCT	ACA	CTT	GGA	GTG	AAA	GAT	GAA	GTT	CTC	2053
230	Gln	Leu	Ile	Thr	Leu	Leu	Ser	Thr	Leu	Gly	Val	Lys	Asp	Glu	Val	Leu	
231	605						610					615				620	
233	GAA	CAG	AAG	CAA	AAG	GAA	GCT	GTA	GAT	CAG	CTT	GAT	GCT	ATC	TTG	CAT	2101
234	Glu	Gln	Lys	Gln	Lys	Glu	Ala	Val	Asp	Gln	Leu	Asp	Ala	Ile	Leu	His	
235						625						630				635	
237	GAT	TCT	TTG	AAG	GCA	CAG	GAG	GCT	TTG	GAA	TTG	ATG	TCT	CCT	GGA	GAG	2149
238	Asp	Ser	Leu	Lys	Ala	Gln	Glu	Ala	Leu	Glu	Leu	Met	Ser	Pro	Gly	Glu	
239				640						645					650		
241	AAC	ACT	AAT	ATT	CTC	AAG	GCA	ATG	CTA	AAC	TGT	GGT	TAT	AAG	CCT	GAT	2197
242	Asn	Thr	Asn	Ile	Leu	Lys	Ala	Met	Leu	Asn	Cys	Gly	Tyr	Lys	Pro	Asp	
243				655						660					665		
245	GCT	GAG	CCC	TTT	CTT	TCA	ATG	ATG	TTG	CAA	ACC	TTC	CGC	GCA	TCC	AAG	2245
246	Ala	Glu	Pro	Phe	Leu	Ser	Met	Met	Leu	Gln	Thr	Phe	Arg	Ala	Ser	Lys	
247				670						675					680		
249	TTG	CTC	GAT	TTG	CGG	ACT	AGA	TCA	AGA	ATA	TTT	ATT	CCA	AAT	GGA	AGA	2293
250	Leu	Leu	Asp	Leu	Arg	Thr	Arg	Ser	Arg	Ile	Phe	Ile	Pro	Asn	Gly	Arg	
251	685						690					695				700	
253	ACA	ATG	ATG	GGA	TGT	TTG	GAT	GAA	TCC	AGA	ACC	TTG	GAA	TAT	GGT	CAG	2341
254	Thr	Met	Met	Gly	Cys	Leu	Asp	Glu	Ser	Arg	Thr	Leu	Glu	Tyr	Gly	Gln	
255						705					710					715	
257	GTG	TTT	GTT	CAG	TTT	ACT	GGT	GCT	GGA	CAT	GGA	GAG	TTT	TCT	GAC	GAT	2389
258	Val	Phe	Val	Gln	Phe	Thr	Gly	Ala	Gly	His	Gly	Glu	Phe	Ser	Asp	Asp	
259				720						725					730		
261	TTA	CAT	CCA	TTT	AAT	AAC	AGC	AGA	TCC	ACC	AAC	AGT	AAT	TTC	ATT	CTG	2437
262	Leu	His	Pro	Phe	Asn	Asn	Ser	Arg	Ser	Thr	Asn	Ser	Asn	Phe	Ile	Leu	
263				735						740					745		
265	AAG	GGA	AAT	GTG	GTT	GTT	GCA	AAA	AAT	CCA	TGC	TTG	CAT	CCT	GGT	GAT	2485

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266	Lys	Gly	Asn	Val	Val	Val	Ala	Lys	Asn	Pro	Cys	Leu	His	Pro	Gly	Asp	
267		750					755					760					
269	ATT	CGT	GTT	TTA	AAG	GCT	GTA	AAT	GTT	CGA	GCG	CTG	CAC	CAC	ATG	GTA	2533
270	Ile	Arg	Val	Leu	Lys	Ala	Val	Asn	Val	Arg	Ala	Leu	His	His	Met	Val	
271	765					770				775						780	
273	GAT	TGT	GTT	GTA	TTC	CCT	CAG	AAA	GGA	AAA	AGA	CCT	CAT	CCG	AAT	GAA	2581
274	Asp	Cys	Val	Val	Phe	Pro	Gln	Lys	Gly	Lys	Arg	Pro	His	Pro	Asn	Glu	
275					785					790						795	
277	TGT	TCT	GGG	AGT	GAT	TTG	GAT	GGG	GAT	ATC	TAC	TTT	GTT	TGC	TGG	GAT	2629
278	Cys	Ser	Gly	Ser	Asp	Leu	Asp	Gly	Asp	Ile	Tyr	Phe	Val	Cys	Trp	Asp	
279					800				805					810			
281	CAA	GAC	ATG	ATC	CCG	CCA	AGG	CAA	GTC	CAG	CCG	ATG	GAA	TAT	CCT	CCA	2677
282	Gln	Asp	Met	Ile	Pro	Pro	Arg	Gln	Val	Gln	Pro	Met	Glu	Tyr	Pro	Pro	
283			815					820					825				
285	GCA	CCC	AGC	ATA	CAG	TTG	GAC	CAT	GAT	GTC	ACA	ATT	GAG	GAA	GTT	GAA	2725
286	Ala	Pro	Ser	Ile	Gln	Leu	Asp	His	Asp	Val	Thr	Ile	Glu	Glu	Val	Glu	
287		830					835						840				
289	GAG	TAC	TTC	ACC	AAC	TAT	ATT	GTG	AAT	GAC	AGT	TTG	GGA	ATC	ATA	GCA	2773
290	Glu	Tyr	Phe	Thr	Asn	Tyr	Ile	Val	Asn	Asp	Ser	Leu	Gly	Ile	Ile	Ala	
291	845					850				855						860	
293	AAT	GCC	CAT	GTC	GTA	TTT	GCA	GAC	AGA	GAA	CCT	GAT	ATG	GCC	ATG	AGT	2821
294	Asn	Ala	His	Val	Phe	Ala	Asp	Arg	Glu	Pro	Asp	Met	Ala	Met	Ser		
295					865				870					875			
297	GAT	CCA	TGC	AAA	AAA	CTT	GCT	GAG	CTC	TTT	TCA	ATT	GCA	GTG	GAC	TTT	2869
298	Asp	Pro	Cys	Lys	Lys	Leu	Ala	Glu	Leu	Phe	Ser	Ile	Ala	Val	Asp	Phe	
299					880				885					890			
301	CCA	AAG	ACT	GGT	GTT	CCC	GCT	GAA	ATA	CCA	TCT	CAG	TTG	CGC	CCT	AAA	2917
302	Pro	Lys	Thr	Gly	Val	Pro	Ala	Glu	Ile	Pro	Ser	Gln	Leu	Arg	Pro	Lys	
303			895					900					905				
305	GAA	TAC	CCA	GAC	TTC	ATG	GAT	AAG	CCG	GAC	AAG	ACC	AGC	TAT	ATC	TCA	2965
306	Glu	Tyr	Pro	Asp	Phe	Met	Asp	Lys	Pro	Asp	Lys	Thr	Ser	Tyr	Ile	Ser	
307		910					915					920					
309	GAA	AGA	GTT	ATT	GGA	AAG	CTT	TTC	AGG	AAA	GTG	AAG	GAC	AAA	GCA	CCT	3013
310	Glu	Arg	Val	Ile	Gly	Lys	Leu	Phe	Arg	Lys	Val	Lys	Asp	Lys	Ala	Pro	
311	925					930				935						940	
313	CAG	GCT	AGC	TCT	ATC	GCG	ACC	TTC	ACA	AGA	GAT	GTT	GCA	AGG	AGA	TCA	3061
314	Gln	Ala	Ser	Ser	Ile	Ala	Thr	Phe	Thr	Arg	Asp	Val	Ala	Arg	Arg	Ser	
315					945				950					955			
317	TAT	GAT	GCT	GAT	ATG	GAA	GTT	GAT	GGA	TTT	GAA	GAT	TAC	ATT	GAC	GAA	3109
318	Tyr	Asp	Ala	Asp	Met	Glu	Val	Asp	Gly	Phe	Glu	Asp	Tyr	Ile	Asp	Glu	
319					960				965					970			
321	GCT	TTT	GAC	TAC	AAA	ACT	GAA	TAT	GAC	AAC	AAG	CTG	GGT	AAT	TTA	ATG	3157
322	Ala	Phe	Asp	Tyr	Lys	Thr	Glu	Tyr	Asp	Asn	Lys	Leu	Gly	Asn	Leu	Met	
323			975					980					985				
325	GAC	TAC	TAT	GGC	ATA	AAA	ACA	GAG	GCT	GAA	ATA	CTT	AGT	GGT	GGC	ATT	3205
326	Asp	Tyr	Tyr	Gly	Ile	Lys	Thr	Glu	Ala	Glu	Ile	Leu	Ser	Gly	Gly	Ile	
327		990					995					1000					
329	ATG	AAG	GCA	TCA	AAA	ACT	TTT	GAC	CGC	AGA	AAA	GAT	GCT	GAG	GCC	ATT	3253
330	Met	Lys	Ala	Ser	Lys	Thr	Phe	Asp	Arg	Arg	Lys	Asp	Ala	Glu	Ala	Ile	

VERIFICATION SUMMARY

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L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]